FIG. 1

Sequence	MB DNA (%)	EC DNA (%)	fold (MB/EC)
GGCGCC=	0.1462	0.0020	73.12
GCCGGC=	0.2317	0.0062	37.19
GTCGAC=	0.0990	0.0116	8.56
CTCGAG=	0.0299	0.0038	7.96
CCCGGG=	0.0645	0.0091	7.13
CACGTG=	0.0205	0.0030	6.74
CCCGAG=	0.0451	0.0069	6.58
CTCGGG=	0.0392	0.0068	5.75
GCCGAC=	0.1435	0.0297	4.83
GTCGGC=	0.1400	0.0295	4.74
CTCGGC=	0.1021	0.0217	4.71
GCCGAG=	0.1000	0.0218	4.58
GACGAG=	0.0493	0.0120	4.10
GCCGCG=	0.1781	0.0435	4.09
GACGTC=	0.0619	0.0151	4.09
GTCGAG=	0.0677	0.0166	4.08
GTCGTC=	0.0755	0.0192	3.93
CTCGAC=	0.0643	0.0165	3.90
CCCGAC=	0.0676	0.0175	3.86
CTCGTC=	0.0501	0.0130	3.86
CGCGGC=	0.1751	0.0455	3.85
GTCGGG=	0.0627	0.0165	3.79
TCCGAG=	0.0203	0.0054	3.78
GACGAC=	0.0747	0.0199	3.76
CTCGGA=	0.0202	0.0054	3.73
GCCGCC=	0.2336	0.0654	3.58
GCCGTC=	0.1008	0.0296	3.41
GGCGGC=	0.2237	0.0662	3.38
GCCGGT=	0.1302	0.0402	3.24
CCCGGC=	0.1183	0.0365	3.24
GACGGC=	0.1033	0.0327	3.16
CCCGCG=	0.0824	0.0263	3.13
GCCGGG=	0.1165	0.0373	3.13
CGCGGG=	0.0849	0.0273	3.11
ACCGGC=	0.1242	0.0405	3.07
GGCGGG=	0.0982	0.0323	3.04
CCCGCC=	0.0995	0.0329	3.02
CGCGGT=	0.1117	0.0372	3.00
ACCGCG=	0.1090	0.0368	2.97
ACCGAG=	0.0511	0.0175	2.92
GTCGGA=	0.0331	0.0118	2.80
GGCGAC=	0.1005	0.0360	2.80
CTCGGT=	0.0494	0.0178	2.78
GTCGCC=	0.1056	0.0383	2.76
GTCGCG=	0.0884	0.0323	2.74
CACGTC=	0.0430	0.0158	2.73
TCCGAC=	0.0326	0.0121	2.70
CGCGAC=	0.0852	0.0320	2.66
Average	0.0498	0.0288	
Sum	12.7440	7.3665	

FIG. 2

a)

MB-ODN 4/5 (-CGXXCGXXXCG-)

No.	Sequence	Score
1	CTCCAcgGGcgGCAcgGCCA	11811
2	TGTCTcgGGcgGCAcgGTTG	11773
3	CAAGGcgGTcgGCTcgATGG	11538
4	AACTGcgGAcgTGGcgGCAG	10931
5	GTCAGcgGAcgTGGcgGCTC	10829
6	AAAGGcgTGcgGGTcgGCCC	10697
7	CTCAGcgGGcgGCAcgTGCA	10670
8	CACAAcgGGcgCCTcgGCTT	10319
9	ATGAAcgGGcgGCTcgAGCC	10240
10	GATGGcgATcgGCAcgCCCA	10199
11	CAGCAcgTGcgTGGcgGCAT	9962
12	GCTGGcgGGcgAGGcgATTC	9855
13	TGTTGcgCTcgGCTcgGCAG	9839
14	GGTGGcgGTcgAGGcgCTCT	9728
15	GGTGGcgCAcgCCTcgGCCC	9259
16	GGGGGcgGTcgCCTcgCTRA	9250
17	GACATcgGTcgGCAcgTCAG	9098
18	CCAGTcgGGcgGGGcgCTGG	9022
19	TCTGGcgGTcgAAGcgGCCC	8953
20	CAACTcgATcgGGGcgCCCA	8878
21	TTTGGcgGTcgGTGcgCAGC	8869
22	CCAGGcgGTcgGTGcgCAGG	8869
23	CTCCTcgGTcgAGGcgGTGG	8844
24	ACCATcgGGcgCCAcgTCTC	8780
25	CAACAcgATcgTGTcgGCTG	8615
...	...	...
353	GTGTTcgAAcgCTAcgAACC	1681
354	AAGTAcgAAcgATGcgAGAA	1637
355	ACTAGcgTAcgCAGcgAATC	1539

b)

MB-ODN 5/5 (-CGXXXCGXXXCG-)

No.	Sequence	Score
1	TGCTcgTGGcgGCTcgGCAG	12868
2	GAGGcgGCTcgGTGcgGGTC	12599
3	TTGGcgGCAcgCAAcgCCTC	11345
4	GAAGcgTTGcgGGGcgGCCC	11280
5	AAGGcgTGGcgGCTcgTGGA	11258
6	CAGGcgATGcgCCTcgGCTC	10614
7	GTTGcgGGAcgAGTcgGCAT	10297
8	GGGGcgGGTcgACTcgACCA	10243
9	TGGTcgGGGcgGGTcgACTC	10153
10	ATCAcgCTAcgGGGcgGCCA	10063
11	GTGGcgCCAcgAGTcgACAT	10059
12	AAGGcgGCTcgCATcgATGG	10036
13	GAGGcgGGGcgGGTcgATCT	9743
14	AATTcgTGGcgGCTcgTGCA	9712
15	CAGGcgGTGcgGTGcgGCAT	9657
16	TAGGcgCTTcgAGTcgGCAC	9655
17	GTGAcgTCAcgGGTcgGCAG	9390
18	GCTTcgAGTcgGCAcgCCAG	9269
19	GTGTcgGGGcgAGGcgACCA	9164
20	TTGGcgTTGcgTGTcgGCCT	9034
21	TCATcgATGcgGGGcgCCAC	8959
22	GAGGcgGGGcgGGGcgGAGA	8873
23	TAGGcgATGcgCAGcgCCTG	8845
24	CAGGcgGTGcgGCAcgCAGT	8703
25	CTGAcgCCTcgGCTcgAGCT	8642
...	...	...
352	ATTAcgCTGcgAAAcgCAGT	1807
353	TAATcgGAAcgTAAcgATCC	1713
354	CATGcgTAAcgTTAcgGAAA	1219

FIG. 3

a)

MB-ODN 4/5 (-CGXXCGXXXCG-)

ODN	Sequence
MB-ODN4/5-1	CCAGTCGGCCGGGGCGCTGC
MB-ODN4/5-2	GCTGGCGGGCCAGGCGATTC
MB-ODN4/5-3	ACCAGCGGGCGAGTCGCCTG
MB-ODN4/5-4	GGTGGCGGGCGTTCGCATC
MB-ODN4/5-5	GGCAGCGGCCCATCGCCAC
MB-ODN4/5-6	CTTGCCGGCGCTCGACCA
MB-ODN4/5-7	AACTGCGACGTGCGCGCAC
MB-ODN4/5-8	GGTCACGGTCGGATCGATTC
MB-ODN4/5-9	TTTGGCGGTCGGTGCGCAGC
MB-ODN4/5-10	GGTGGCGGTCGAGCGCTCT
MB-ODN4/5-11	GGTGGCGGTCGAGCGCTCT
MB-ODN4/5-12	TTTGTCGGTCGCAACGAAAA
MB-ODN4/5-13	GATGTCGAGCGGATCGGCAC
MB-ODN4/5-14	TTGCTCGAGCGGTTCGGCAT
MB-ODN4/5-15	TTGGTCGAGCGTGTCGGGTC
MB-ODN4/5-16	ACCATCGAGCGCAGCGTGGT
MB-ODN4/5-17	GGCAGCGAGCGCAACGACAC
MB-ODN4/5-18	CTCATCGAGCGCCACGGCAC
MB-ODN4/5-19	ATGCTCGAGCGCCTCGGCCC
MB-ODN4/5-20	GGCTTCGAACGGGTCGAGGG
MB-ODN4/5-21	GATGCCGAACGTGACGTCAT
MB-ODN4/5-22	CTTGTCGAACGTCTCGGCCA
MB-ODN4/5-23	GAGATCGAACGCTTCGACAC
MB-ODN4/5-24	CAGTTCGATCGAGACGACCC
MB-ODN4/5-25	GTAGGCGATCGATGCGCGAA
MB-ODN4/5-26	CAACACGATCGTCTCGGCTC
MB-ODN4/5-27	CTAGGCGATCGCAACGAAGT
MB-ODN4/5-28	CCACACGATCGCCACGGTGC
MB-ODN4/5-29	GGCAGCGTGCGTGACCACTT
MB-ODN4/5-30	TAAGGCGTGCCCATCGATAT
MB-ODN4/5-31	AGCAGCGTTCGTCTCGCCCT
MB-ODN4/5-32	TGTTGCCGACGGTGCGCTGC
MB-ODN4/5-33	CTGGGCCGACGCGACGCTGG
MB-ODN4/5-34	GGCAGCCGACGCAGCCGAAC
MB-ODN4/5-35	GCAGGCGCTCGTCACGCCCC

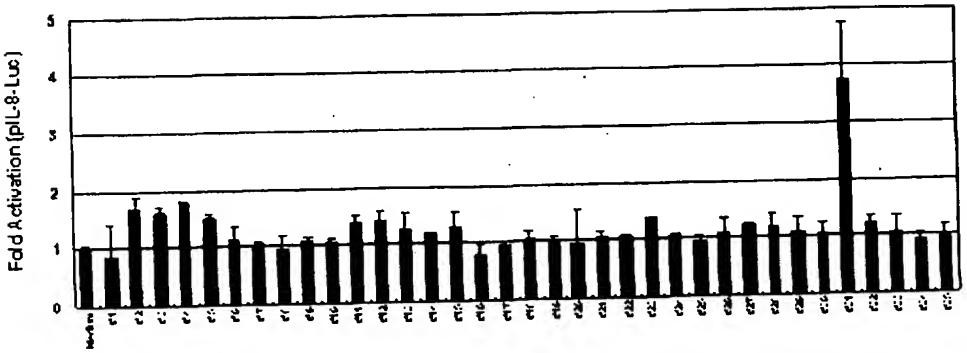
b)

MB-ODN 5/5 (-CGXXXCGXXXCG-)

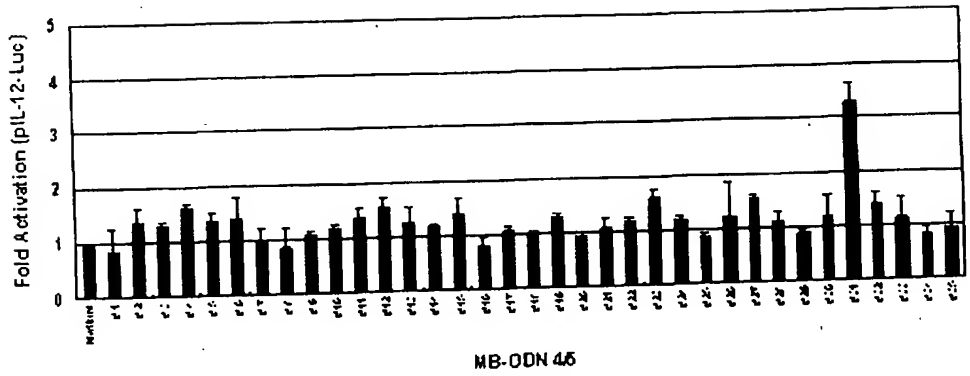
ODN	Sequence
MB-ODN5/5-1	GATGCCGATCGGTGCGCTGC
MB-ODN5/5-2	CAGGCGGTGCGCAACGCCTG
MB-ODN5/5-3	GATGCGGTGCGCATCGCCAA
MB-ODN5/5-4	GAGGCGGTGCGCCACGTGCT
MB-ODN5/5-5	GCAGCGGCTCGACACGACAA
MB-ODN5/5-6	TGGTCGAGCGGTTGCGGCAC
MB-ODN5/5-7	ACAGCGAGTCGCTGCGCCAC
MB-ODN5/5-8	TAGGCGAAGCGATCGCGCCC
MB-ODN5/5-9	TCAGCGAAGCGGTGCGCCCA
MB-ODN5/5-10	ATCTCGAAGCGCTGCGAGGG
MB-ODN5/5-11	GGGTCGAATCGTGTCGCCTC
MB-ODN5/5-12	TAGGCGATGCGCAGCGCCTG
MB-ODN5/5-13	ATGGCGATGCGCTGCGCCTG
MB-ODN5/5-14	GGGTCGACACGCTGCGATTG
MB-ODN5/5-15	TGCTCGTGCGGGTCTGGCAG
MB-ODN5/5-16	CCAGCGTGGCGATGCGGCGA
MB-ODN5/5-17	GCATCGTGGCGCAGCGCATG
MB-ODN5/5-18	TGGACGTGTCGTAGCGCAGG
MB-ODN5/5-19	CTGGCGTAGCGCCTCGCCGT
MB-ODN5/5-20	TTGGCGTTGCGTGTCGGCGT
MB-ODN5/5-21	AAATCGTTGCGGCACGCGAT
MB-ODN5/5-22	ATCACGTTGCGCAGCGGGTG
MB-ODN5/5-23	AAATCGTCTCGAGCGTTCC
MB-ODN5/5-24	GTGGCGCACGCGTCGCGCTGG
MB-ODN5/5-25	TGGCGCGACGCGCACGCTAT
MB-ODN5/5-26	TCTCGCGACGCGATCGTTCA
MB-ODN5/5-27	TGGCGCGACGCGTACGAACT
MB-ODN5/5-28	GCGTCGCAGCGACACGTTGC
MB-ODN5/5-29	TTGGCGCAACGCGATCGCGA
MB-ODN5/5-30	GCAGCGCAACGCTTGCGCATC
MB-ODN5/5-31	ACAACGCATCGCGATCGAGCA
MB-ODN5/5-32	ACCACGCTGCGGCGTCGTCAC
MB-ODN5/5-33	ACTGCGCTGCGCGACGACCC
MB-ODN5/5-34	GTCTCGCTGCGCAGCGGGGT
MB-ODN5/5-35	GGCACGCTGCGTCACGTCGT
MB-ODN5/5-36	CTCACGCCTCGCGTCGAGCT

FIG. 4

a)


Fold Activation (pIL-8-Luc)
0
1
2
3
4
5
MB-ODN 46

b)


Fold Activation (pIL-12-Luc)
0
1
2
3
4
5
MB-ODN 46

c)

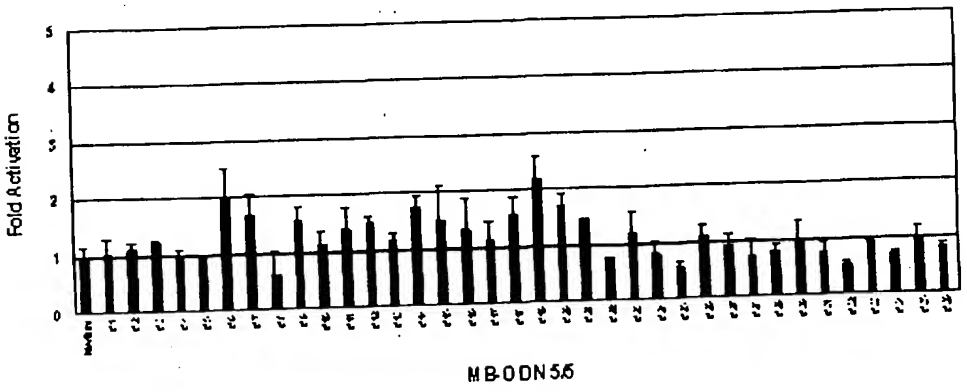

Fold Activation
0
1
2
4
5
MB-ODN 56

FIG. 5

a)

ODN	Sequence
MB 4/5 #31	AGCAGCGTTCGTGTCGGCCT
#31.1	CAGCTCGTTCGTGTCGTGCT
#31.2	TGTGGCGTTCGTGTCGGTCT
#31.3	TGCAACGTTCGTGTCGCCAC
#31.4	GGCCACGTTCGTGTCGGTAG
#31.5	GAACACGTTCGTGTCGGAAC
#31.6	CAGCACGTTCGTGTCGGACA
#31.7	TATGTCGTTCGTGTCGTCTT
#31.8	AAGGGCGTTCGTGTCGCTTG
#31.9	ATTTGCGTTCGTGTCGATTC
#31.10	GGTGGCGTTCGTGTCGTCAT
#31.11	ATGGGCGTTCGTGTCGATCC
#31.12	GTATTCGTTCGTGTCGTCCT
#31.13	GGGAACGTTCGTGTCGGTGC
#31.14	TGACTCGTTCGTGTCGCATG
#31.15	GTCATCGTTCGTGTCGAGAC
#31.16	TTGCACGTTCGTGTCGATGA
#31.17	CAGCACGTTCGTGTCGGTCA

b)

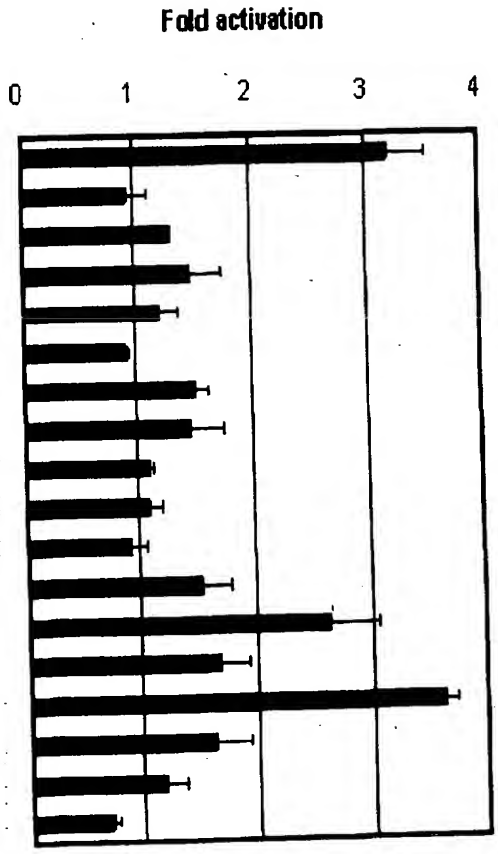


FIG. 6

a)

ODN	Sequence
MB-ODN 31(O)	AGCAGCGTTCGTGTCGGCCT
MB-ODN 31(M)	AGCGTTCGTGTCGGC
#31-CG-1	AGCAGGCTTCGTGTCGGCCT
#31-CG-2	AGCAGCGTTGCTGTCGGCCT
#31-CG-3	AGCAGCGTTCGTGTGCGCCT
#31-CG-4	AGCAGGCTTGCTGTCGGCCT
#31-CG-5	AGCAGGCTTCGTGTGCGCCT
#31-CG-6	AGCAGCGTTGCTGTGCGCCT
#31-CG-7	AGCAGGCTTGCTGTGCGCCT
#31-A-1	AGCAGCATTCGTGTCGGCCT
#31-A-2	AGCAGCTTTCGTGTCGGCCT
#31-A-3	AGCAGCCTTCGTGTCGGCCT
#31-B-1	AGCAGCGTTCATGTCGGCCT
#31-B-2	AGCAGCGTTCTTGTCGGCCT
#31-B-3	AGCAGCGTTCCTGTCGGCCT
#31-C-1	AGCAGCGTTCGTGTCAGCCT
#31-C-2	AGCAGCGTTCGTGTCTGCCT
#31-C-3	AGCAGCGTTCGTGTCCGCCT
#31-D-1	AGCAGCATTCATGTCGGCCT
#31-D-2	AGCAGCATTCGTGTCAGCCT
#31-D-3	AGCAGCGTTCATGTCAGCCT

b)

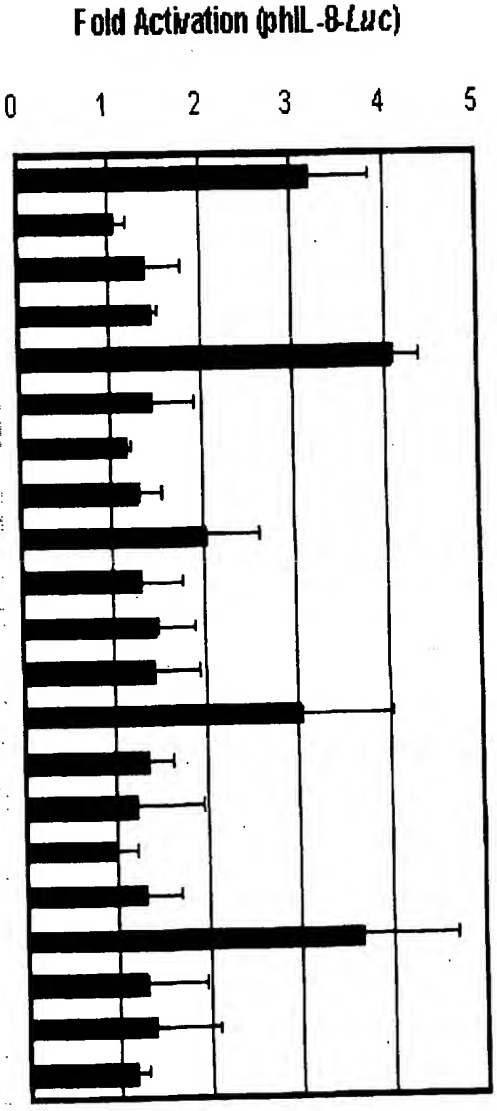


FIG. 7

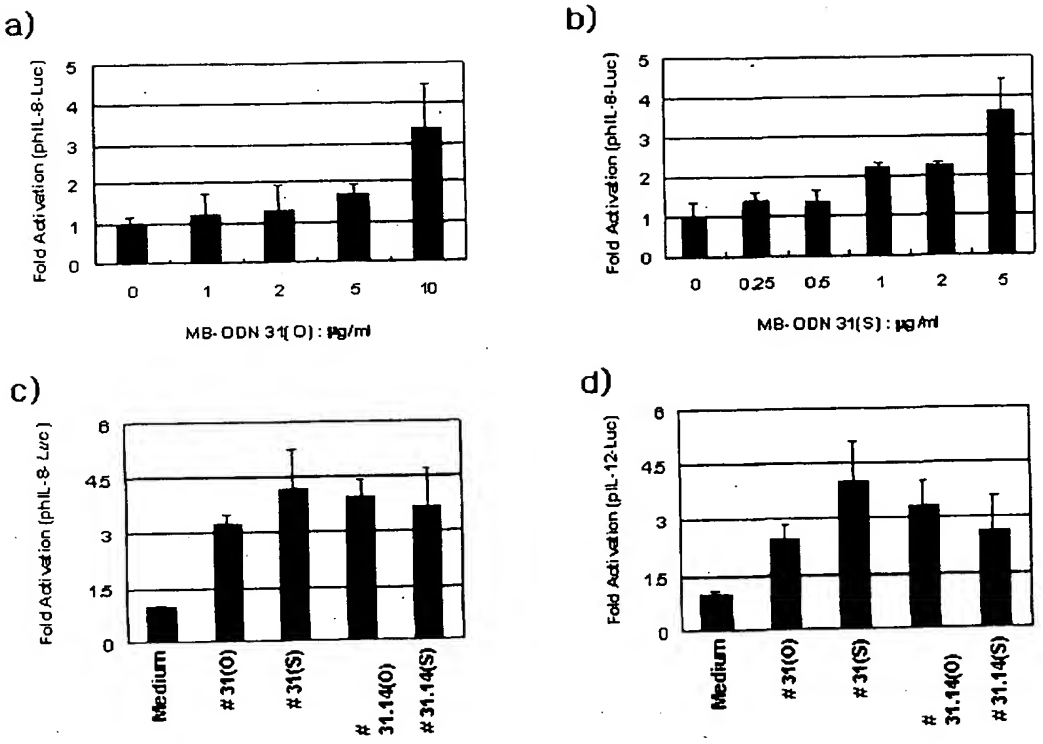
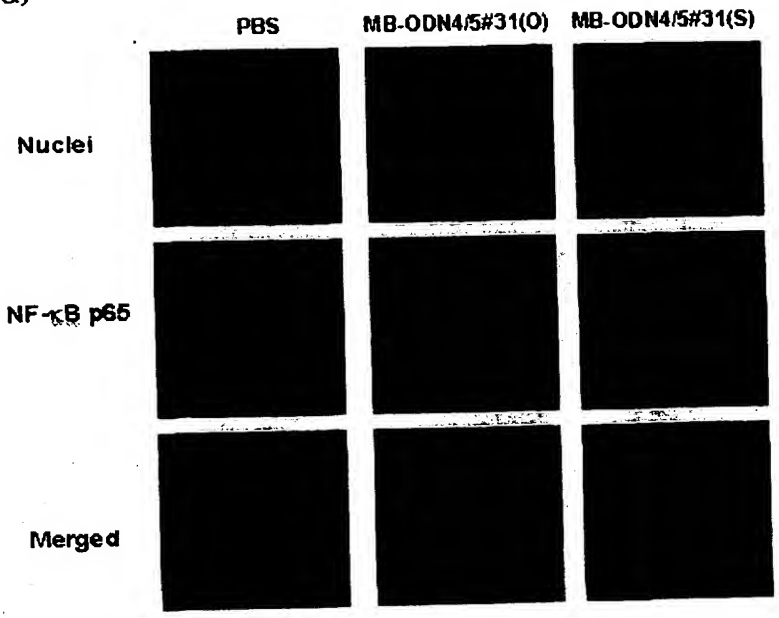

a)
Fold Activation (phIL-8-Luc)
0
1
2
3
4
5
0
1
2
5
10
MB-ODN 31(O) : μg/ml
b)
Fold Activation (phIL-8-Luc)
0
1
2
3
4
5
0
0.25
0.5
1
2
5
MB-ODN 31(S) : μg/ml
c)
Fold Activation (phIL-8-Luc)
0
1.5
3
4.5
6
Medium
#31(O)
#31(S)
31.14(O)
31.14(S)
d)
Fold Activation (pIL-12-Luc)
0
1.5
3
4.5
6
Medium
#31(O)
#31(S)
31.14(O)
31.14(S)

FIG. 8

a)


PBS
MB-ODN4/5#31(O)
MB-ODN4/5#31(S)
Nuclei
NF-κB p65
Merged

b)

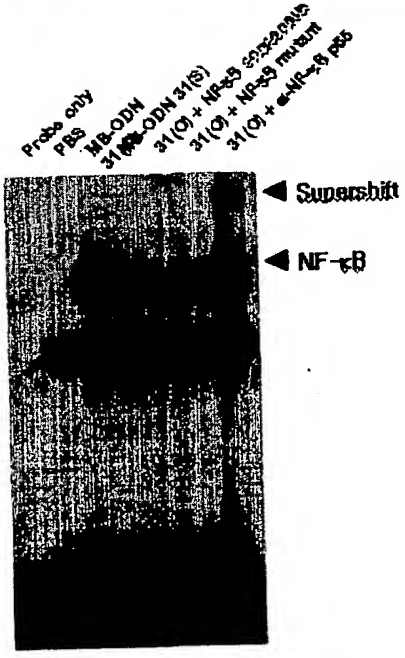

Probe only
PBS
MB-ODN
31(S)
MB-ODN 31(S)
31(O) + NF-κB consensus
31(O) + NF-κB mutant
31(O) + α-NF-κB p65
Supershift
NF-κB

FIG. 9

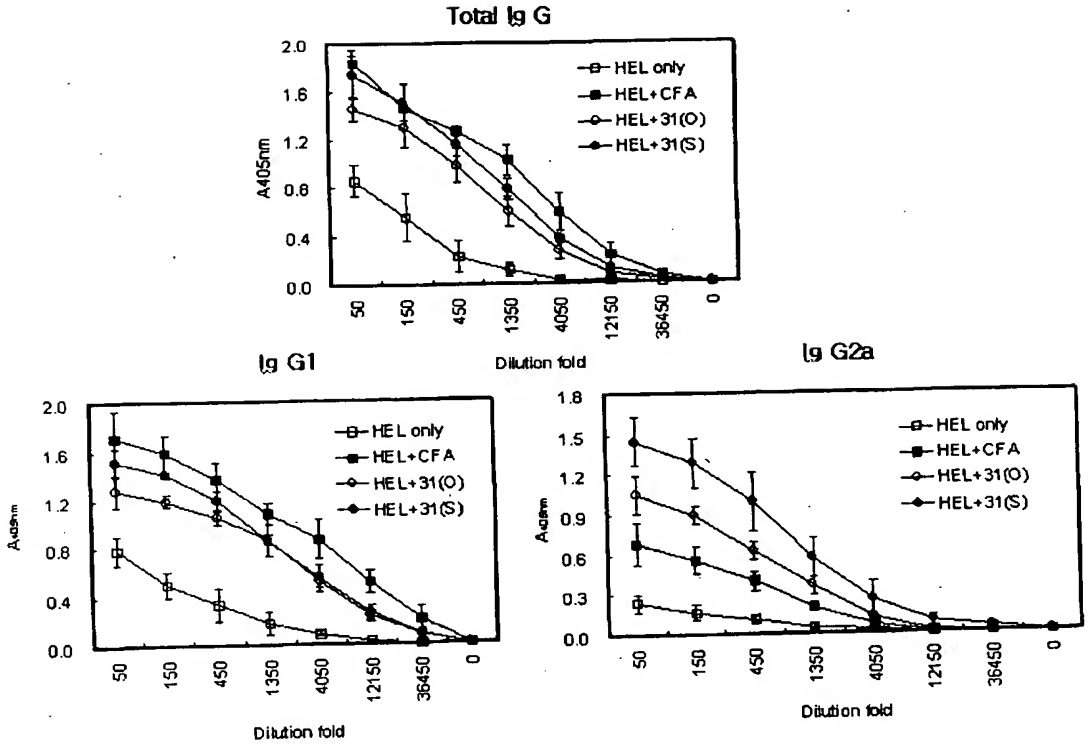

Total Ig G
A405nm
HEL only
HEL+CFA
HEL+31(O)
HEL+31(S)
Dilution fold
Ig G1
Ig G2a

FIG. 10

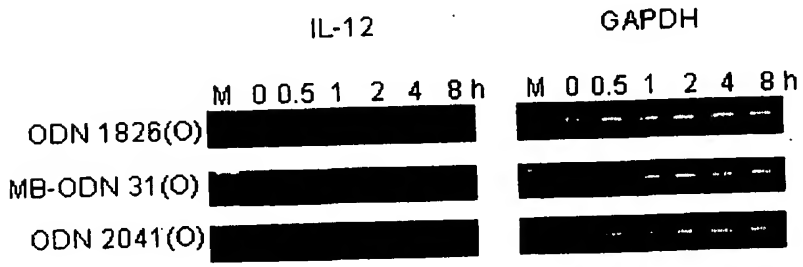

IL-12
GAPDH
M 0 0.5 1 2 4 8 h
ODN 1826(O)
MB-ODN 31(O)
ODN 2041(O)

FIG. 11

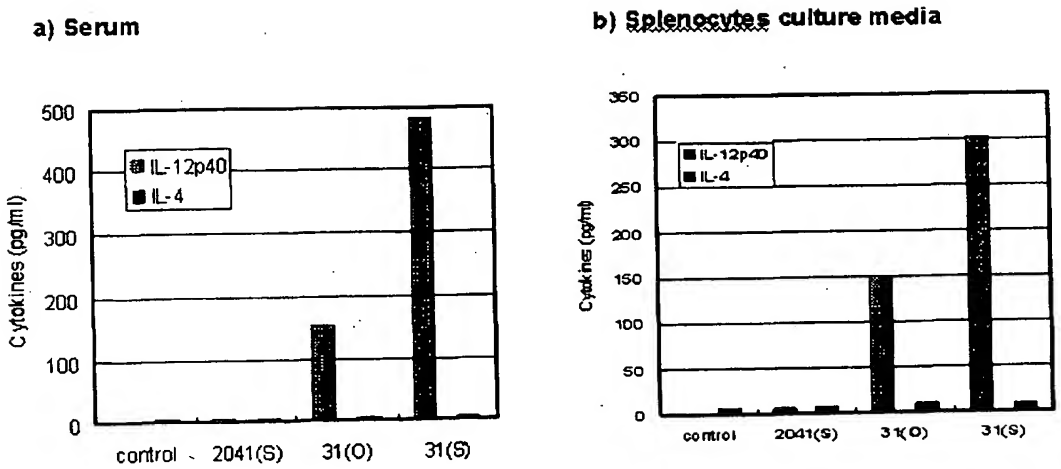

a) Serum
b) Splenocytes culture media
Cytokines (pg/ml)
IL-12p40
IL-4
500
400
300
200
100
0
control
2041(S)
31(O)
31(S)
360
300
250
200
150
100
50
0

FIG. 12

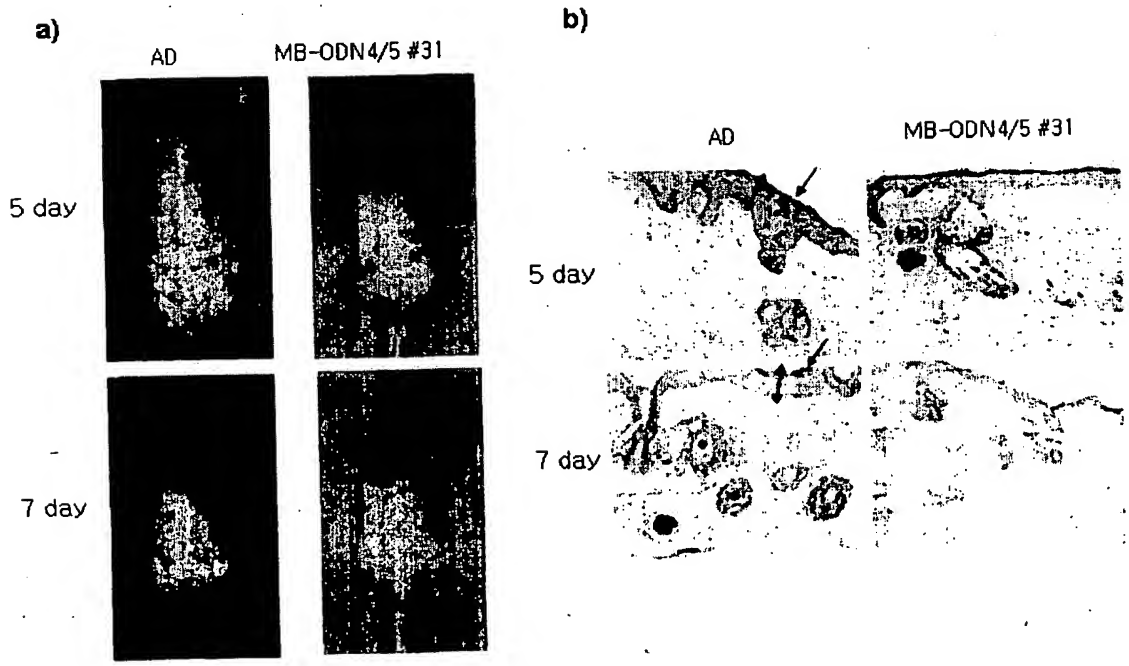

a)
AD
MB-ODN4/5 #31
5 day
7 day
b)
AD
MB-ODN4/5 #31
5 day
7 day

FIG. 13

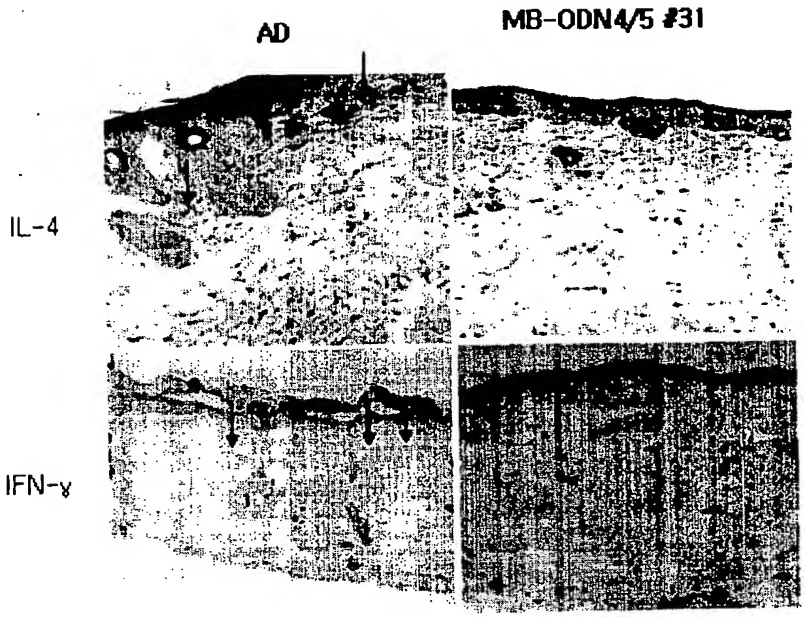


FIG. 14

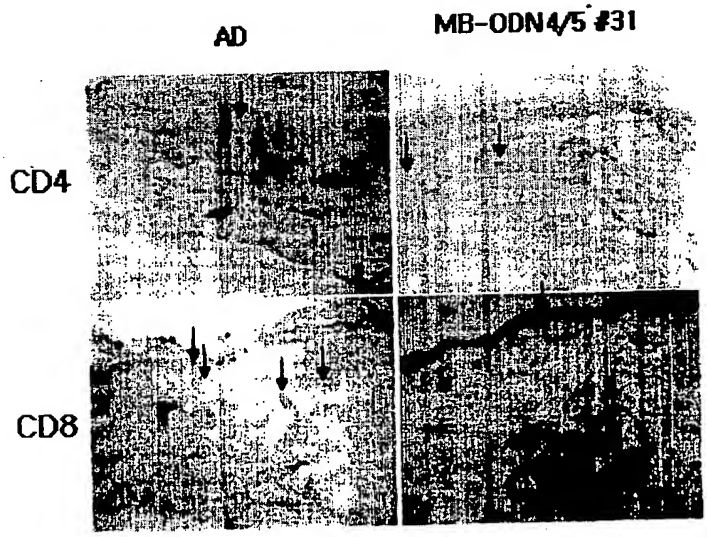


FIG. 15

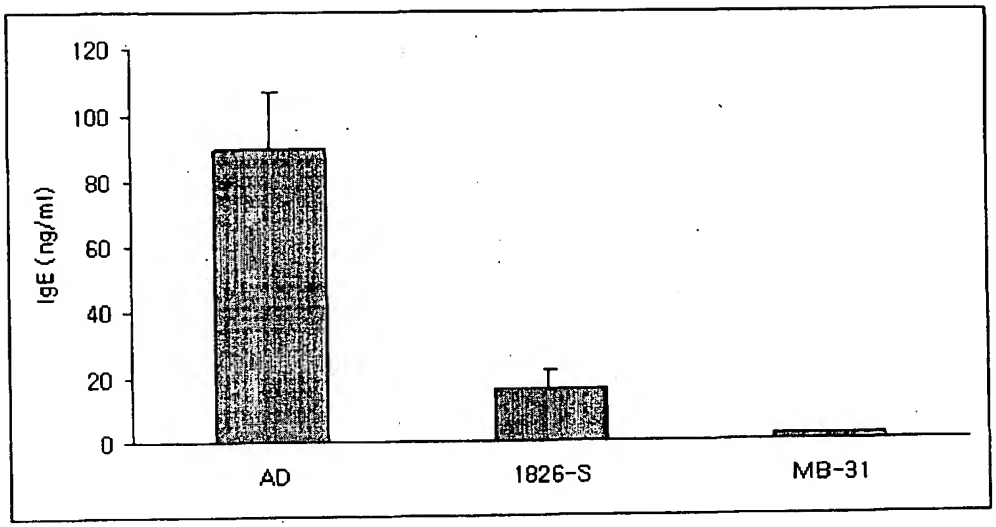

120
100
80
60
40
20
0
IgE (ng/ml)
AD
1826-S
MB-31

FIG. 16

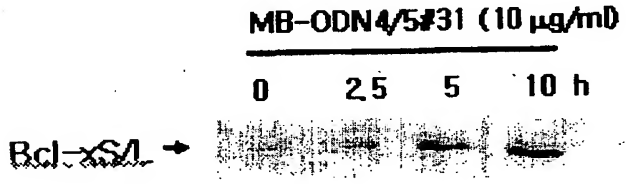

MB-ODN4/5#31 (10 μg/ml)
0
2.5
5
10 h
Bcl-xS/L

FIG. 17

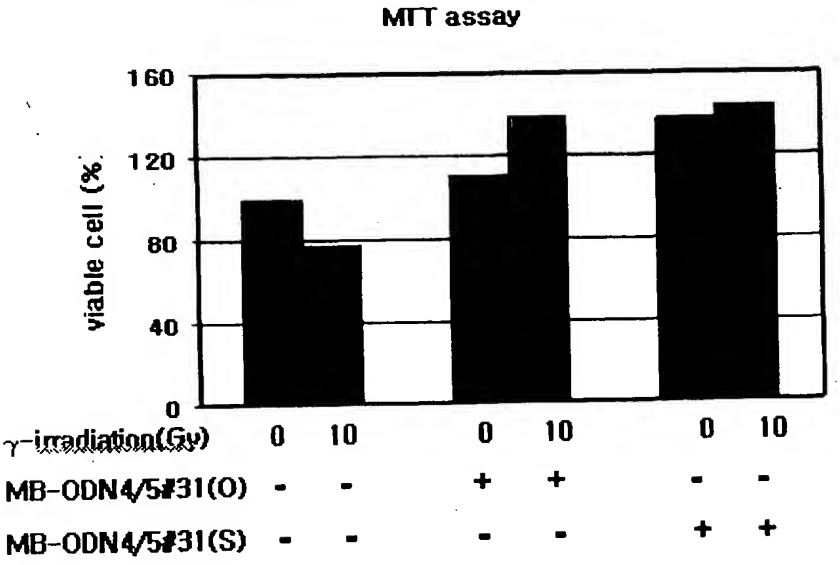

MTT assay
viable cell (%)
160
120
80
40
0
γ-irradiation(Gy) 0 10 0 10 0 10
MB-ODN4/5#31(O) - - + + - -
MB-ODN4/5#31(S) - - - - + +

FIG. 18

A) Control, 0 Gy B) Control, 10 Gy C) MB-ODN4/5#31(S), 10Gy

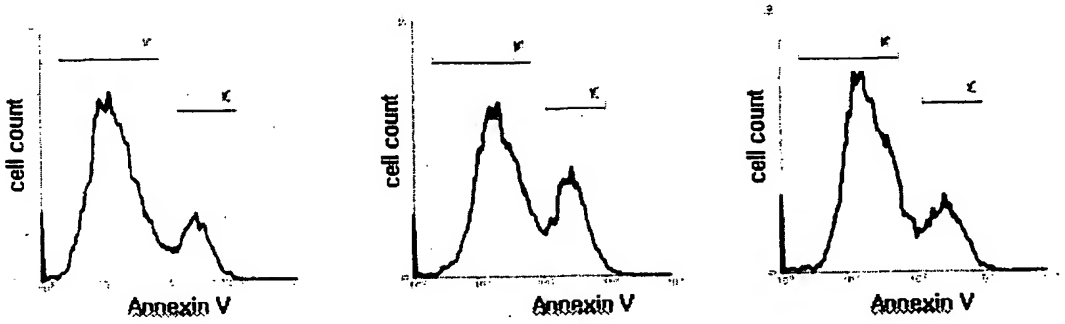
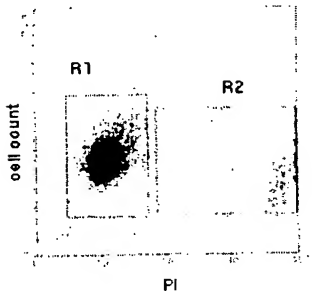


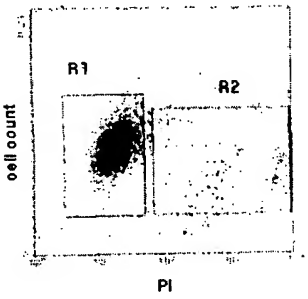
Fig.	γ -Irradiation	MB-ODN 4/5 #31(S)	Marker	%Total
A	0 Gy	(-)	M1 M2	73.54 16.709
B	10 Gy	(-)	M1 M2	58.82 27.24
C	10 Gy	(+)	M1 M2	65.25 18.71

FIG. 19

A) Control, 0 Gy



B) Control, 10 Gy



C) MB-ODN4/5#31(S), 10Gy

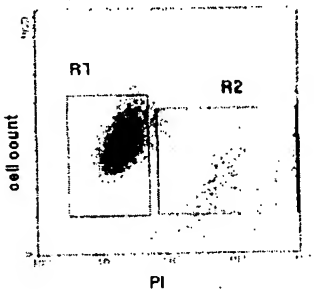


Fig.	γ - irradiation	MB-ODN 4/5 #31(s)	Region	%Total
A	0 Gy	(-)	R1 R2	73.30 16.32
B	10 Gy	(-)	R1 R2	58.93 25.33
C	10 Gy	(+)	R1 R2	62.82 20.92